

**Amendments to the claims:**

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a ~~substantially~~ purified ~~AviIII peptide~~ polypeptide with cellulase activity and having at least 90 ~~99%~~ identity to SEQ ID NO. 1, ~~said AviIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.~~
2. (Currently Amended) The composition of claim 1 wherein the ~~polypeptide AviIII peptide is further defined as comprising~~ comprises a glycosyl hydrolase family 74 (GH74\_Ace) enzyme, a carbohydrate binding domain (CBD) III, a linker, and a signal sequence.
3. (Cancelled)
4. (Currently Amended) The composition of claim ~~1 or 2~~ wherein the carbohydrate binding domain (CBD) III of the polypeptide ~~AviIII peptide~~ is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Currently Amended) The composition of claim ~~1 or 2~~ wherein the carbohydrate binding domain (CBD) III of the polypeptide ~~AviIII peptide~~ is further defined as comprising a length of about 90 amino acids.
6. (Currently Amended) The composition of claim ~~4~~ 2 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide of sequence identical to ~~SEQ ID NO: 3.~~

7. (Currently Amended) The composition of claim 4 2 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Currently Amended) The composition of claim 4 2 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Currently Amended) The composition of claim 4 2 wherein said polypeptide ~~AviIII protein~~ comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10-11. (Cancelled)

12. (Currently Amended) ~~An isolated~~ A purified polypeptide ~~AviIII~~ peptide-having at least 99% identity to a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Currently Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the ~~AviIII~~ polypeptide of claim 1.

15. (Previously presented) The industrial mixture of claim 14 further defined as comprising a detergent.

16-27 (Cancelled)

28. (Currently Amended) ~~An isolated~~ A purified polypeptide having at least 99% identity to molecule comprising at least one a polypeptide sequence selected from the group consisting of:

a) ~~a polypeptide sequence of~~ SEQ ID NO: 3;

b) ~~a polypeptide sequence of~~ SEQ ID NO: 4;

- c) ~~a polypeptide sequence of SEQ ID NO: 5; and~~  
d) ~~a polypeptide sequence of SEQ ID NO: 1; and~~  
~~— e) combinations thereof.~~
29. (Cancelled)
30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.
31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.
32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.
33. (Previously presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.
34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.
35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.
36. (Currently Amended) A cellulase-substrate complex comprising the ~~isolated polypeptide molecule~~ of claim 28 bound to cellulose.
- 37-42 (Cancelled)
43. (Currently Amended) A composition comprising the polypeptide ~~molecule~~ of claim 28 and a carrier.
- 44-46. (Cancelled)

47. (Currently Amended) The composition of claim 1 wherein said catalytic domain of GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII\_Aac):

GH74_Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWKNVVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG *:.*.***.*. **** *. ***** .* *: *.***** ** :: : * **.***
GH74_Ace	WNNWGYNGVVSIAADPINTNKVWAAVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMYTNEWDPNVGSILRSTDQGDWTETKLPFKVVG :.* *: :*:*:*:*:*:*.*****.***** *:*****:*** ** * *****:
GH74_Ace	GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSTFTWTGTYFDSSS *****:*****:***** **:*:***:*** *****:*. . .***: :.:
GH74_Ace	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNNPVFWSRDGGATWQAVPGAP-T
AviIII_Aac	T--YTSDPVGIAWVTFDSTSGSSGSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY * * * * *:.*:*.*:*. * *: *****.:.** *.***** *.* *
GH74_Ace	GFIPHKGVFDPVNVHLYIATSNITGGPYDGGSDVWKFVSTSGTWTRISPVSTDTANDYF
AviIII_Aac	GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNTSGVWTDISP---TSLASTYY **:*:***:.* :*:***: * .*****:. * * *:.*:***.* ** * . * . *:
GH74_Ace	GYSGLTIDRQHPNTIMVATQISWPDITIFRSTDGGATWTRIWDWTSYPNRSRLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCWWPEDELIFRSTDGATWSPIWEWNGYPSINYYYSYDIS **.*:.* * *.*:***: .***** :*****.*****: **:*..* . * ***
GH74_Ace	AEPWLTFGVQPNPPVPSPKLGWMDAAMIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac	NAPWIQDITSTDQFP--VRVGWVMEALADPFDSNHWLYGTGLTVYGGHDLTNWDSKHNV ** : . . . : :*** **:*:***:***: ***** *. . :***:*** ::
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSTV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPGGPALLSAVGDDGGFYHSDLAAPNQAYHTPTYGTNGI : . . *:* * * .*:*.*.*.*:*** ** * *: * . : :*: * .:
GH74_Ace	DYAEINPSIIVRAGSFDPSQPNDRHVAFTDGGKNWFQGGSEPGGVTTGGTVAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT *** :** ***:*. * . :*:*: *..*: . . * *:* ** *
GH74_Ace	FVWAPGDPGPVVYAVGFGNSWAASQGVPAQAIRSDRVNPKTFYALSNGTFYRSTDGGV
AviIII_Aac	VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSGAGAIYVSKNTAT : . . * * * : * : * .*:*. * * * : .** . * : * * .:
GH74_Ace	TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGGSSWSAI-TGVSSAVNV
AviIII_Aac	SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF :* . . : * * *:.*: * * .***: * :.***:***: ***: * :***: . .
GH74_Ace	GFGKSAPGSSYPVAVFVGTIGGVTGAYRSDDCGTTWVLINDDQHGYGN-WGQAITGDHAN
AviIII_Aac	GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT ****:. .** :. . **.*: * :*:*.***. * :.* * . :. :.*** .
GH74_Ace	LRRVYIGTNGRGIVYGDIGGAPSG
AviIII_Aac	YGRVFRGHERPGHLLRQSREPAG ** : * : * : : *:* .

48. (Currently Amended) The composition of claim 47 wherein said ~~AviIII~~ peptide polypeptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (Currently Amended) A composition comprising a ~~substantially~~ purified ~~AviIII~~ peptide polypeptide having at least ~~99~~95% identity to SEQ ID NO. 1, said ~~AviIII~~ peptide polypeptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (Currently Amended) The composition of claim 49 wherein said catalytic domain of GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AviIII\_Aac):

GH74_Ace	ATTQPYTWSNVAIGGGG-FVDGIVFNAGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG
AviIII_Aac	AASQAYTWKNVVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG
	*:*.***.*. **** *. ***** .* *: *.***** ** :. : * **.***
GH74_Ace	WNNWGYNGVVSIAADPINTNKVWAAVGMVYNSWDPNHGAILRSSDQGATWQITPLPFKLG
AviIII_Aac	NDTWHDWGIDALATDPVDTDRVYVAVGMVYNSWDPNHGAILRSSDQGATWQITPLPFKLG
	:. * * :. :*.***:*.***:*.*****.***** *.***** ** * *****:
GH74_Ace	GNMPGRGMGERLAVDPNNDNILYFGAPSGKGLWRSTDGATWSQMTNFPDVGTYIANPTD
AviIII_Aac	GNMPGRGMGERLAVDPNKNILYFGARSGHGLWKSTDYATWSNVTSTFTWTGTYFQDSSS
	*****.*****:*.***** **.*.***** *****:*. * .****. :. :.
GH74_Ace	TTGYQSDIQGVVWVAFDKSSSSLGQASKTIFVGVADPNPVPFWSRGGATWQAVPGAP-T
AviIII_Aac	T--YTSDPVGIAWVTFDSTSGSSGATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPQY
	* * * * *:*.***:*. * * *: *****. :. * * *.***** * * *
GH74_Ace	GFIPHKGVFDPVNHVLYIATSNITGGPYDGSSGDVWKFVSTSGTWTRISPVPSTDTANDYF
AviIII_Aac	GFLPHKGVLSPEEKTLYISYANGAGPYDGTNGTVHKYNITSGVWTDISP--TSLASTYY
	**.*.*****:*. * :.***: * * .*****: * * *:*.***** ** * * * *
GH74_Ace	GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGATWTRIWDWTSYPNRSRLRYVLDIS
AviIII_Aac	GYGGLSVDLQVPGTLMVAALNCWPELIFRSTDGATWSPIEWNGYPSINYYSYDIS
	**.*.***: * * *.***: .***** :*****.*****: **.*.***. . * **
GH74_Ace	AEPWLTFGVQPNPPVPSPKLGWMDAAMIDPFNSDRMLYGTGATLYATNDLTKWDSGGQI
AviIII_Aac	NAPWIQDTTSTDQFP--VRVGWVVEALAIIDPFNSDRMLYGTGATLYATNDLTKWDSKHN
	** : . . . : :*** **.*.*****:*. ***** *: . :***.*** :.
GH74_Ace	HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTSTV
AviIII_Aac	TVKSLAVGIEEMAVLGLITPPGGPALSAVGDDGGFYHSDLDAAFNQAYHTPTYGTNGI
	: . . . *.* ** .***.***.***:*** ** * *: * . : :. : * . . .
GH74_Ace	DYAEINPSIIVRAGSFDPSQPNDRHVAFSTDGKKNWFQSGEPGGVTTGGTVAASADGSR
AviIII_Aac	DYAGNKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAASTSTGTGAVALSADGDT

51. (Currently Amended) The composition of claim 50 wherein said ~~peptide~~ polypeptide retains at least the same level of cellulase activity and oral tolerability as those exhibited by the peptide of SEQ ID NO. 1.

53. (Currently Amended) A composition comprising a substantially purified AvIII-peptide polypeptide, said AvIII-peptide polypeptide comprising characterized by a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain of GH74\_Ace having a sequence that is at least ~~90~~ 99% identical to SEQ ID NO. 3.

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55. (New) A composition comprising a genetically engineered polypeptide expressed in a heterologous host cell, said polypeptide having at least 99% identity to SEQ ID NO. 1.

56. (New) A composition comprising a genetically engineered polypeptide expressed in a heterologous host cell, said polypeptide comprising a sequence having at least 99% identity to SEQ ID NO. 3.